	Total	N	m
	IOCAL	N-Clones (208F-FE-8)	T-Clones (FE8-208F)
Number of sequenced cDNA clones	1257	669	588
Number of individual sequences	823	416	407
Sequence analysis			
Known genes (nr/Genbank)	427	207	220
Expressed Sequence Tags (dbest)	303	161	142
No similarity in data bases (new)	93	48	45
Expression analysis: Reverse Northern Analysis/con- ventional Northern Blot			
Differentially expressed	393	225	168
Known genes	244	126	118
Expressed sequence tags	104	74	30
New sequences	45	25	20
Not differentially expressed	194	86	108
Not detectable in expression analysis	236	105	131

FIG. 1

Genes that are adjusted down by H-Ras-transformation

Genes that are adjusted up by H-Ras-transformation

				Extent				-		Extent	
				Jo						Jo	
		Access Redund- Adjust- Verif-	-pun	Adjust-	·Verıf-		À	Access Redund- Adjust-Verif-	-pun	Adjust-	Verif-
Sequence Identity (Genbank/EMBL)	Species	Number ar	ancy	ment	ment ication	Sequence Identity (Genbank/EMBL)	Species N	Number ancy	сy	ment	ication
				ίς.	ıgnalling	Signalling Molecule					
3',5'-cyclic AMP phosphodiesterase	ы	222867	-	>100	NI	AKAP-KL (A kınase anchor protein)	m	AF033276	-	16.1	T1,R
AhR repressor	E	AB015140	~	38.0	∝.	B61 (eck receptor ligand)	H	38056	П	5.2	T2
CAMP-dependent protein kinase type II	ы	M12492	Н	>100	œ	c-Hn-ras-1	'n	700574	H	17.0	Т3
CSF-1 (colony stimulating factor-1)	ы	M84361	7	5.6	N2, R	c-yes	E	767677	_	12.5	T 4
Gas-6	Ħ	X59846		24.0	œ	Calmodulin-dependent protein kinase II-delta	ы	305072	П	8.1	œ
Guanine nucleotide-binding protein G-s alpha	ы	M12673	Н	3.6	N3	Cyclooxygenase I	n n	103388		7.06	T5,R
I-TRAF (TRAF-interacting protein)	E	MMU59864	-	38.6	N4	Cytocentrin=Ral-binding protein 1	ı,	128830	1		16
IKK-complex-associated protein (IKAP)	.c	AF014195		9.8	24	FKBP51 (T-cell specific immunophilin)	:) E	116959	1	68.2	T7
MARCKS	E	M60474	7	3.3	NS	FLIP (FLICE-like inhibitory protein)	;) E	970760	7	>100	18
MST2 kinase	ы	AJ001529	7	21.6	<u>~</u>	GEF-HI	<u>ب</u>	172206	-	32.1	T9
Myo-inositol monophosphatase (IMP)	ы	U84038	-	44.5	9N	GTP-binding protein RAB5	zi zi	F072935	-	>100	110
P5 protein	ha	X62678		3.4	æ	JAKI protein-tyrosine kinase l	H	1000556	_	55.0	T11
Phosducin-like protern (PhLP)	ы	L15354	7	>100	N7,R	MAP-kinase phosphatase (cpg21)	r J	AF013144	-	27.9	T12,R
Phosphatidylinositol 3-kınase p110 beta	٦	S67334	П	>100	N8	p67 (isoprenylated 67 kDa protein)	Ħ	M80367	 1	98.2	T13
Phosphatidylinositol 3-kınase p170	E	U55772	-	62.9	N9, R	Phosphatase 2A B56	٦ ۲	42373	7	50.6	T14
Protein tyrosine phosphatase delta (MPTPd)	E	D13903	-	1.9	œ	PkB kinase	H	X15748	-	19.9	T15
ROK alpha	ы	U38481	-	26.1	N10	R-esp2	u u	14463	-	>100	T16
Serum inducible kinase (SNK)	E	M96163	ч	>100	N11,R	RaplB GTP binding protein	n H	007795	Н	21.0	T17
SH3 binding protein (SAB)	ч	AB005047	H	3.5	œ	Ras-GTPase-activating protein	m A	AB001927	-	9.9	T18
						RhoC	E	X80638	7	6.7	œ
						SBF1 phosphatase	n u	093181		27.1	T19,R
					•	Sprouty 2 (SPRY2)	h A	AF039843	7	11.60	T20,R
					•	TDAG51	D E	044088	\vdash	2.7	T21
						Tyrosine phosphatase IA-2a	r D	D38222	П	12.2	T22

FIG. 2

	z	Nuclear Proteins	eins	(Trans	sription	Transcription Factors, DNA Processing Enyzmes)					
AHNAK nucleoprotein	ᄱ	M80902	2	>100	N12	Alpha-prothymosin	ы	M60664	\vdash	2.4	α;
ATP-dependent RNA helicase	E	U46690	-	0	N13	BRCA1-associated RING domain protein (Bard1)	E	AF057157		3.5	T23
BRG-1 (brahma homolog)	E	S68108	_	13.1	N14	cdc-like-kinase (clk)	E	L29221	\leftarrow	13.1	T24
CCAAI/enhancer binding (C/EBP gamma)	Ħ	X64403	-	16.6	N15	FEN-1 (flap endonuclease-1)	E	L26320		11.1	T25
Cdc21	E	D26089	-	3.9	α;	Fra-1 (fos-related antigen 1)	ы	M19651	m	>100	T26,R
Centromeric protein CENPC	E	U03113	_	39.5	N16, R	Histone acetyltransferase (GCN5)	ď	AE029777	.	2.7	T27
Chromosome-associated polypeptide C(CAP-C)	Ч	AB019987	-	9.6	œ	hNop56 nucleolar protein	,c	Y12065	Н	5.9	T28
DNA polymerase epsilon	Ч	AF036899	-	5.1	α.	LAP1C (lamina-associated polypeptide 1C)	ы	U19614		7.6	T29
DNA repair protein RAD50	E	U66887	Н	3.4	N17, R	Myb-binding protein (P160)	E	U63648		ი. ე.	T30
ERS1 transcription factor	Ч	U17163	-	9.6	N18	NF-1 transcription factor	E	U57635	, 1	71.8	T31
ETF TEA domain containing transcription factor	E	D50563	-	7.4	N19	pl00 transcriptional coactivator	Ч	U83883	, ,	4.9	α.
Gu binding protein	ч	U78524	ч	41.7	N20	PEBP2b2	E	D14571	7	45.4	T32
HEC retinoblastoma-associated protein	ц	AF017790	ч	3.9	N21,R	RB (retinoblastoma protein)	ы	D25233	-	6.5	T33
Helicase p68 (HUMP68)	Ţ	AF015812	7	>100	N22, R	SA-1 (stromal antigen)	E	Z75332	, ,	89.1	T34,R
Histone H3.3	ď	Z48950	7	5.8	œ						
Ki-67 antigen	Ε	X82786	-	>100	N23, R						
LAP2 (Lamina associated polypeptide 2)	H	U18314	4	>100	N24,R						
Mouse zinc finger protein	E	D45210	-	5.6	N25						
mTFE3 (X-linked transcriptional activator)	E	S76673	-	3.6	œ						
Nuclear autoantigen GS2NA	ď	U17989	П	31.9	œ						
Nucleoporin 155	ч	AJ007558	-	15.2	N26						
Poly(ADP-ribose) glycohydrolase (hPARG)	E	AF079557	П	2.4	œ						
Rnf4 transcription factor	E	U95141	7	64.9	œ						
Single strand DNA-binding protein	ď	AF077048	_	4.9	~						
STAT5al transcription factor	ы	U24175	1	1.8	N27						
Topoisomerase I	E	D10061	,—ł	20.1	œ						
Topoisomerase II	Ħ	Z19552	m	2.1	œ						
	Pr	otein Proce	ssing	, Prot	ein Trans	rotein Processing, Protein Transport and Protein-folding Molecule	=				
26S proteasome subunit p55	æ	AB003103		3.5	N28	Aminopeptidase P(APP)	ч	AF038591	2	5.6	œ
GRP94/endoplasmin	E	\$69316	1	2.2	œ	Chaperonin containing TCP-1 epsilon(CCT)	E	Z31555	7	2.2	T35, R
Heat shock protein 105	E	D67016		15.1	N29	Exportia	ч	AF039022	4	48.5	_T36
Heat shock protein 90	.C	X15183		4.8	N30, R	GRP75	ы	878556	5	2.4	S. A. S.
										i de la companya de l	

FIG. 2A

onspo	N32 NEPP Sec6 Sort Sort Transporter R 4F2h R 4F2h N33 ASV N34 ASV N34 ASV N35 Blee N35 Elec N35 Elec	MPDB (mirochondrial processing peptidase beta) MPDB (mirochondrial processing peptidase beta) Social Social Sortilin) Translation initiation factor 3 Arghers and Ion Channels AFZhe intestinal type II membrane glycoprotein ABC transporter MOAT-B Acyl-CoA synthetase 1 Aldehyde reductase Asparagine synthetase	ненсс нск	L12965 S83456 M96630 X98248 U94855	- T - T - T	4.3 19.7 29.2	6X E
Metabolic Enzymes, Transpor r X52625 2 12.7 R r J03637 1 37.8 N33 m X61172 1 6.3 R m U9646 1 1.8 N34 m S56599 1 58.7 R h U76713 1 >100 N35 r X79328 2 4.7 N36 r M8751 1 18.8 N37 h D78014 1 2.3 R r X13220 1 5.3 R r X13220 1 5.3 R r X13220 1 5.3 R r U90556 1 6.2 N39	Ran- Sec6 Sort Transporter R 4F2h R 4F2h R 4F2h R ASC N33 ACyl R ASD N34 ASD N35 Blec N35 CIC- N37 Fame	JTPase [(sortilin) slation initiation factor 3 slation Litiation factor 3 s and Ion Channels e intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	हमयद मयम	\$83456 M96630 X98248 U94855 U59324	7 7	19.7	L C E
Metabolic Enzymes, Transport X52625 2 12.7 R 1 03637 1 37.8 N33 M X61172 1 6.8 N34 M S56599 1 58.7 R N N79328 2 4.7 N36 N37 N N3655 1 1 2.3 R N N37 N N3655 1 1 2.5 R N N3220 1 5.3 R N N3220 1 12.3 N38 R N6374 2 31.8 N40	Sec6 Sort Tran Es, Transporter R 4F2h N33 A92 R A79 R A104 R A104 N35 B1ec N36 CIC-	l (sortilin) slation initiation factor 3 sand Ion Channels e intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	HEE HER	M96630 X98248 U94855 U59324	7	29.5	127
Metabolic Enzymes, Transport X52625 4 5.0 R 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	es, Transporter R 4F2h R 4F2h R 4F2h R 4F2h N33 ASU N34 ASU N34 ATP N35 Blec N36 CIC-	l (sortilin) slation initiation factor 3 sand Ion Channels e intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	aa Har	X98248 U94855 U59324			T38, R
Metabolic Enzymes, Transpor r S63167 4 5.0 R r X52625 2 12.7 R r J03637 1 37.8 N33 m X61172 1 6.3 R m 96746 1 1.8 N34 m 55639 1 58.7 R h U76713 1 >100 N35 r X79328 2 4.7 N36 r M8751 1 18.8 N37 h D78014 1 2.3 R r X13220 1 5.3 R r X13220 1 5.3 R r U90556 1 6.2 N39 r M6374 2 31.8 N40	es, Transporter R 4F2h R ABC N33 Acyl R Alde N34 ASP N35 Blec N36 CIC-	slation initiation factor 3 s and Ion Channels e intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	d Mar	U94855 U59324		10.5	T39
Metabolic Enzymes, Transport X52625 4 5.0 R r X52625 2 12.7 R r J03337 1 37.8 N33 m X61172 1 6.3 R m U96746 1 1.8 N34 m S56599 1 58.7 R h U76713 1 >100 N35 r X79328 2 4.7 N36 r M88751 1 18.8 N37 h D78014 1 2.3 R r X14848 1 2.5 R r X13220 1 5.3 N8 m Z49204 1 12.3 N38 r M63574 2 31.8 N40	es, Transporter R 4F2h R ABC N33 Acyl R ASpa N34 Aspa R ATP N35 Blec N36 CIC-	s and Ion Channels a intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	د عبيد	U59324		5.7	T40,R
r x52625 2 12.7 R r y52625 2 12.7 R r y0337 1 37.8 N33 m x61172 1 6.3 R m y6746 1 1.6 N34 m x65899 1 58.7 R h y7613 1 >100 N35 r x79328 2 4.7 N36 r x79328 2 4.7 N36 r x79328 1 2.3 R r x1322 1 2.3 R r x1322 1 2.5 R r x1322 1 2.5 R r x1322 1 2.5 R r y1322 1 2.5 R r y1323 1 2.5 R r y1324 1 2.5 R		a intestinal type II membrane glycoprotein transporter MOAT-B -CoA synthetase 1 hyde reductase	ਮਟਮ	059324			
r X52625 2 12.7 R r J03637 1 37.8 N33 m X61172 1 6.3 R m U96746 1 1.8 N34 h U76113 1 >100 N35 r X79228 2 4.7 N36 r M88751 1 18.8 N37 h D78014 1 2.3 R r X13220 1 5.5 R r X13220 1 5.5 R r X13220 1 5.3 R r U90556 1 6.2 N39 r M63574 2 31.8 N40		cransporter MOAT-B -CoA synthetase 1 hyde reductase ragine synthetase	e r		작	2.9	T41
r J03637 1 37.8 N33 m X61172 1 6.3 R m U96746 1 1.8 N34 h U76113 1 >100 N35 r X79228 2 4.7 N36 r X88751 1 18.8 N37 h D78014 1 2.3 R r X14848 1 2.5 R r X13220 1 5.3 R m Z49204 1 12.3 N38 r U90556 1 6.2 N39		-CoA synthetase 1 hyde reductase ragine synthetase	3.	AF071202		10.8	T42,R
M X61172 1 6.3 R M U96746 1 1.8 N34 M U76713 1 58.7 R F X79228 2 4.7 N36 F X89751 1 18.8 N37 F M91652 3 10.4 R F X13220 1 5.3 R F M63574 2 31.8 N40		hyde reductase ragine synthetase	4	D30666	-	4.1	œ
m U96746 1 1.8 N34 m S56599 1 58.7 R h U76713 1 >100 N35 r X79228 2 4.7 N36 r M8751 1 18.8 N37 h D78014 1 2.3 R r M91652 3 10.4 R r X14848 1 2.5 R r X14848 1 2.5 R r X14848 1 2.5 R r X14846 1 2.5 R r X14856 1 5.3 R r W63574 2 31.8 N40		ragine synthetase	ы	D10854	1	4.0	T43
m S56599 1 58.7 R h U76713 1 >100 N35 r X79328 2 4.7 N36 r M88751 1 18.8 N37 h D78014 1 2.3 R r X14848 1 2.5 R r X14220 1 5.3 R m Z49204 1 12.3 N38 r U90556 1 6.2 N39 r M63574 2 31.8 N40			ы	007201	4	15.3	œ
r X79328 2 4.7 N36 r M88751 1 18.8 N37 N36 r M88751 1 18.8 N37 N36 r M91652 3 10.4 R r r X14848 1 2.5 R r r X14848 1 2.5 R r r X13220 1 5.3 R r r M9556 1 6.2 N39 r M63574 2 31.8 N40		NTP citrate-lyase	ы	J05210	7	3.1	œ
r X79328 2 4.7 N36 r M88751 1 18.8 N37 h D78014 1 2.3 R r r M91652 3 10.4 R r r X14848 1 2.5 R r r x13220 1 5.3 R r r x13220 1 5.3 R r r w63574 2 31.8 N40		3leomyein hydrolase	ы	D87336	7	8.	T44,R
r M88751 1 18.8 N37 h D78014 1 2.3 R r r M91652 3 10.4 R r r X14848 1 2.5 R r r X13220 1 5.3 R r r M9556 1 12.3 N38 r M63574 2 31.8 N40		<pre>SIC-6a (chloride channel)</pre>	æ	X99473	_	19.6	ρζ
h D78014 1 2.3 R r M91652 3 10.4 R r X14284 1 2.5 R r X13220 1 5.3 R m Z49204 1 12.3 N38 r U90556 1 6.2 N39 r M63574 2 31.8 N40		amesyl pyrophosphate synthetase	ч	M34477	2	 	T45,R
r X14848 1 2.5 R C x X13220 1 5.3 R R R Z49204 1 12.3 N38 I r U90556 1 6.2 N39 I R M63574 2 31.8 N40		Glucose-6-phosphate dehydrogenase	뇌	X07467		2.4	ഷ
5		Glutathione reductase	ч	073174	1	2.7	T46, R
6 r X13220 1 5.3 R 249204 1 12.3 N38 1 1 r U90556 1 6.2 N39 1 r M63574 2 31.8 N40 1 1	_	Glvr-1 (leukemia virus receptor 1)	E	M73696	2	22.2	œ
m 249204 1 12.3 N38 1 n n38 1 n n38 1 n n38 1 n n39 1 n	_	MCT1 monocarboxylate transporter	ч	X86216	-	7.5	œ
osphohydromse type 2		Mitochondrial trifunctional protein	ы	D16478	~	2.4	T47
r M63574 2 31.8 N40	_	Non-neuronal enolase (NNE)	ы	X02610	ι'n	2.5	œ
	N40 NPC-	1 protein	E	AF003348	-	3.1	æ
	Phos	Phosphoglycerate mutase type B	ы	863233	4	5.6	<u>«</u>
Stenroyl-(Sten	Stenroyl-CoA desaturase 2	ы	AF036761	, 1	7.5	œ
Transcript	Tran	ranscript ass. with monocyte differentation	.с	X85750	_	8.2	T48
Transports	Tran	Pransporter protein (917)	.ц	U49082	_	4.2	ps;
X-chromose	x-ch	X-chromosome linked phosphoglycerate kinase	ы	M31788		2.9	œ



FIG. 2B

ABP-280 (actin-binding protein/filamin) h X53416 Alpha-actin Cadherin-11 Cadherin-12 Cytohesin-2 Gas-1 HSPG core fibroglycan (syndecan-2) r W81687 huEMAP microtubule associated protein r W004434 MLC-2 P-cadherin r W6349 Podoplanin r W6340 Podoplanin r W64723 Vimentin r X62952	116 1001 557 119 . 33 128 119 . 144434 114434 114443 11444 114443 11444 11444 114443 114443 114443 11444 114	5.8 4.2 111.7 37.7 >10.0 10.9 61.9 26.9 2.6	R R N41 N42 N43,R N44 N45,R	Arp3 (actin-related protein 3) Calcium-binding protein pp52/LSP1/WP34 Calponin C044 glycoprotein Laminin receptor Leukocyte adhesion protein p150,95 MAGE-B gene cluster Myosin regulatory light chain TA1 oncofetal gene Thymosin beta 4		83 3	3.3 29.7 5.2 17.0	149,R 150,R R
rin-11 smon smon ssin-2 ssin-2 m core fibroglycan (syndecan-2) m m core fibroglycan (syndecan-2) m m m rerin erin anin anin rin n rin ri	557 11 119 3 228 11 228 1 144434 1 1440 1 1440 1 1688 1 1687 1 1688 1 16	4.2 111.7 37.7 7.100 10.4 10.4 61.9 2.6 60.1		Calcium-binding protein pp52/LSP1/WP34 Calponin CD44 glycoprotein Laminin receptor Leukocyte adhesion protein p150,95 MAGE-B gene cluster Myosin regulatory light chain TA1 oncofetal gene Thymosin beta 4		7 1 1 5	5.2	150,R
m smon syndecan-2) r r r m m m care fibroglycan (syndecan-2) r r m m m m r r in m m m m m m m m m m m m m m m m m m	11.9 . 12.8 . 12.8 . 12.8 . 13.8 . 14.4 . 14.4 . 14.4 . 14.9 . 14.9	11.7 37.7 >100 10.4 61.9 2.6 60.1		Calponin CD44 glycoprotein Laminin receptor Leukocyte adhesion protein pi50,95 MAGE-B gene cluster Myosin regulatory light chain TA1 oncofetal gene			5.2	ا د د
ssin-2 solin-2 m core fibroglycan (syndecan-2) microtubule associated protein nerin nerin nan nan yosin 4 r r r r r r r r r r r r r	11.19	37.7 >100 10.4 61.9 26.9 2.6 60.1		CD44 glycoprotein Laminin receptor Leukocyte adhesion protein p150,95 MAGE-B gene cluster Myosin regulatory light chain TAl oncofetal gene		, 1	17.0	ć
roce fibroglycan (syndecan-2) m core fibroglycan (syndecan-2) r m retin terin anin anin canin r in r in r in	228 1 228 1 187 1 187 1 14434 1 1400 2 1400 1 1499 1	>100 10.4 61.9 26.9 2.6 60.1		Laminin receptor Leukocyte adhesion protein p150,95 MAGE-B gene cluster Myosin regulatory light chain TAl oncofetal gene				Y'ICI
m m core fibroglycan (syndecan-2) r P microtubule associated protein h rerin m anin canin tyosin 4 r Y/Clusterin r r r r r r r r r r r r r r r r r r r	28 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10.4 61.9 26.9 2.6 60.1		Leukocyte adhesion protein p150,95 MAGE-B gene cluster Myosin regulatory light chain TAl oncofetal gene Thymosin beta 4		2	4.1	œ
core fibroglycan (syndecan-2) r microtubule associated protein h refin m anin anin yosin 4 r r r r r r r r r r r r r	14434 11 1000 2 1490 11 149 11	61.9 26.9 2.6 60.1		MAGE-B gene cluster Myosin regulatory light chain TAl oncofetal gene Thymosin beta 4	h Y00093	7	5.2	ĸ
microtubule associated protein h rerin m anin yosin 4 //clusterin r r r r r r r r r r r r r r r r r r r	14434 1 100 2 140 1 149 1 168 6	26.9 2.6 60.1		Myosin regulatory light chain TAl oncofetal gene Thymosin beta 4	_		15.3	T52
rerin manin ranin yosin 4 ranin rani	100 2 140 1 149 1	2.6		TAI oncofetal gene Thymosin beta 4	r D14688		6.9	α,
anin ranin m ranin sanin ranin kanin	140 1 149 1	60.1		Thymosin beta 4	r 000995	7	4.9	T53
rin r	149 1	Ø			r M34013	-	2.4	T54,R
rin K	9 89							
rin r		5 27.7						
rın	. 69	7.8						
4 3-4	123	39.4						
	152 1	1.6						
		<u>ы</u>	xtracellu	Extracellular Proteins				
Collagen albhal r 278279		34 22.3		MMP-1 (Collagenase)	r M60616		>100	T55,R
e-early dene)				MMP-3 (Stromelysin 1)	r x02601		32.3	T56,R
		4 35.8		MMP-10 (Stromelysin 2)	m X05083	12	33.8	tx;
E				Moh-1	r U17035		2.4	T57, R
				T 100 F			σ, ∞	T58
- I								
11107=12 10111:								
4 E								
0.00		14 9.2	í íz					
to t								
≑ ε		3 6						
ייי								
wth factor) m								
MMP-2 (Gelatinase A) r U65656		3 50.6						
Thrombospondin 1 M62470								
TIMP-2 (inhibitor of metalloproteinase 2) r S72594	194	18,3					``	A WEST

Cytoskeleton Components-Molecule Involved in Adhesion and Cell-Cell Interaction



FIG. 2C

1) h AF002672 1 6.9 T62 3) m AB013607 1 6.4 R	2 3.1 N60 1 1 10.2 R
suppressor candidate 1) h nydroxylase isoform 3)	1 10.2 R 2 7.4 N61,R
3) r M18864 1 2.6 M M M3312 2 2.8 M M3312 2 2.8 M M3312 2 2.8 M M3024704 1 2.3 M M03510 1 12.0 r M05110 1 12.0 r M0510 1 12.0 r M0510 1 1.6 M M19393 1 16.0 h M50717 1 6.0 h M50717 1 6.0 h M50717 1 6.0 h M50717 1 2.9 h M5071169 1 2.9 h M5071169 1 4.2 h M5071169 1 4.2 r KU037376 1 28.7 r KU037376 1 28.7 r KU037376 1 28.7 r KU037376 1 28.7 r M15319 1 55.5 h M88136 3 2.4 m M505979 1 2.3 h M88136 2 2.2 h M88136 2 2.2	10 1 21.3 R
r M19312 2 2.8 r M19312 2 2.8 lon tumors h AB013607 1 6.3.0 lon tumors h AB024704 1 2.3 lon tumors h AB024704 1 2.3 rain gene r AB015345 1 2.9 r W09510 1 1.6 h M19393 1 16.0 h AF064093 1 3.2 h AB001308 1 10.7 h AB001308 1 10.7 h AB01116 1 2.9 h AB01119 1 2.3 h M88136 1 2.2 h AF095791 1 2.3 like brotenn 1A-2a; PTP35 r U40652 11 74.9,5;	2 5.0 R
protein homolog (N1p3) m AF041054 1 63.0 lon tumors h AB024704 1 2.3 lon tumors h M9510 1 12.0 rain gene r U09510 1 12.0 h M19393 1 16.0 h AB005308 1 10.7 h AB007308 1 10.7 h AB011097 1 2.9 h AB011097 1 2.9 h AB011097 1 2.9 h AB011109 1 4.2 h AB011109 1 2.9 h AB011109 1 2.1 h M08136 2 2.2 like brotein 1A-2a; PTP35 r U40652 11 74.9.3;	1 >100 N62
protein homolog (N1p3) m AF041054 1 63.0 lon tumors h AB024704 1 2.3 h AB024704 1 2.3 rain gene r AB015345 1 2.9 r M19393 1 16.0 h AF064093 1 3.2 h AF064093 1 3.2 h AB07130 1 0.7 h AB07130 1 2.9 h AB071105 1 2.1 h AF09595 1 1 2.2 h AF09595 1 2.2 like protein 1A-2a; PTP35 r U40652 11 74,9,5.5	N63, R
lon tumors h AB024704 1 2.3 knobs10 1 12.0 rain gene r AB015345 1 2.9 r 109510 1 12.0 knobs10 1 16.0 knobs10	N64
rain gene r AB015345 1 2.0 rain gene r AB015345 1 2.9 r U09510 1 1.6 h M19393 1 16.0 h AF064093 1 3.2 h AF064093 1 3.2 h AB002308 1 10.7 h AB011097 1 2.5 h AB01116 1 9.4 h AB01116 1 2.5 h AF055889 1 7.3 r RU037376 1 2.9 h M188958 1 1.8 r RU037376 1 2.1 llar alaxia type 3 gene) r Y12319 1 2.2 h M8813 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 ke brotein 1A-2a; PTP35 r U40652 11 74.9,3.	1 3.9 R
rain gene r AB015345 1 2.9 rain gene r 10910 1 1.6 h M1933 1 16.0 h AF064093 1 3.2 h AB002308 1 10.7 h AB001309 1 2.5 h AB01116 1 2.5 h AR05889 1 7.3 r V103736 1 28.7 r V103736 1 28.7 r V10319 1 2.1 h M8015 1 2.2 h AF095791 1 2.3	
1.6	1 >100 N66 H
h M19393 1 16.0 h AF064093 1 3.2 h AB002308 1 10.7 h AB007177 1 6.0 h AB07177 1 6.0 h AB071891 1 2.5 h AB011167 1 2.9 h AB011167 1 2.9 m AB011169 1 4.2 h AB011169 1 4.2 h AB011169 1 4.2 h AF055889 1 7.3 x U60116 1 >100 r XLU37376 1 28.7 r W1088958 1 1.8 r W1088958 1 1.8 r W1088958 1 1.8 r W108958 1 1.	1 16.3
h AF064093 1 3.2 h DS7717 1 6.0 h AB002308 1 10.7 h AB002308 1 10.7 h AB011097 1 2.9 h AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 4.2 h AF055889 1 7.3 x U60116 1 7.3 x U60116 1 7.0 r XLU37376 1 28.7 r RNU88958 1 1.8 r W10832 1 1.8 r W10833 1 9.3 h MW 0053921 2.1 m L13129 1 2.2 h AF095791 1 2.3 r U52945 2 2.2	1 33,8 R
h DS7717 1 6.0 h AB002308 1 10.7 h AB007891 1 2.5 h AB011097 1 2.9 h AB01116 1 2.9 h AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 2.9 h AB01116 1 2.9 h AF055889 1 7.3 x U60116 1 7.3 x U60116 1 7.0 r XLU37376 1 28.7 r XLU37376 1 28.7 r XLU37376 1 28.7 r XLU37376 1 2.1 xta type 3 gene) r Y1Z319 1 55.5 h M88136 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 r U52945 2 2.2 znn 1A-2a; PTP35 r U40652 11 74.9.5.5	1 4.8
h AB002308 10.7 h AB011097 2.9 h AB01116 2.9 h AB01116 9.4 h AB01116 2.9 m AB01116 2.9 m AB01116 1.2 h AF05589 7.3 x U60116 1.29 r XLU37376 1.8 r XLU37319 1.8 r XLU37319 1.3 h NM 0053921 2.1 h M88136 2.2 h AF095791 2.2 h AF095791 2.2 h AF095791 2.2	1 3.6 R
AB007891 1 2.5 h AB01105 1 2.9 h AB01116 1 9.4 h AB01116 1 2.9 m AB01116 1 2.9 m AB01116 1 2.9 h AB01116 1 2.9 h AB01116 1 2.9 x U6016 1 7.3 x U6016 1 7.3 r XLU37376 1 28.7 r XLU37319 1 55.5 h M88136 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 r U52945 2 2.2 sin 1A-2a, PTP35 r U40652 11 74.9.3.	30 1 20.8 R KIAA0431
AB011097 1 2.9 h AB01116 1 9.4 h AB01116 1 9.4 h AB01116 1 2.9 m AB011167 1 2.9 h AF05589 1 7.3 x U6016 1 7.00 r XL037376 1 28.7 r XL03737 1 28.7 r XL03737 1 28.7 r XL03737 1 2.1 h MW 053921 1 2.1 h MW 053921 1 2.2 h AF095791 1 2.3 r U52945 2 2.2 sin 1A-2a, PTP35 r U40652 11 74.9.3.	5 20.2 R KIAA0525
AB01116 1 9.4 h AB011167 1 2.9 m AB011169 1 4.2 h AF055889 1 7.3 x U60116 1 >100 r XLU37376 1 28.7 r RNU88958 1 1.8 r protein) r U41853 1 9.3 h MM 0053921 1 2.1 xia type 3 gene) r Y1219 1 55.5 h AF095791 1 2.3 r U40652 11 74.9.;	~
h AB011167 1 2.9 m AB011169 1 4.2 h AF055889 1 7.3 h AF055889 1 7.3 x U60116 1 >100 subunit (cls1) r XU0137376 1 28.7 r XU0137376 1 28.7 r RU088959 1 1.8 r Q41853 1 9.3 r Q41853 1 2.1 r XI01319 1 2.1 r XI01319 1 2.1 r XI01319 1 2.1 r XI01319 1 2.2 r XI01319 1 2.2 r XI01319 1 2.3 r XI01319	
m AB011169 1 4.2 h AF055889 1 7.3 x UG0116 1 >100 x UG0116 1 >100 r XLU37376 1 28.7 r XLU37376 1 28.7 r RNU88958 1 1.8 r Q41853 1 9.3 h NM O053921 1 2.1 x1a type 3 gene) r Y12319 1 55.5 h M88136 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 r U52945 2 2.2 sin 1A-2a, PTP35 r U40652 11 74.9.	5 2.7 R
A AF055889 1 7.3 x U60116 1 >100 r XLU37376 1 28.7 r XLU37376 1 28.7 r RNU88958 1 1.8 r Q41853 1 9.3 h M0053921 2.1 x1a type 3 gene) r Y12319 1 2.5 h M8813 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 r U52945 2 2.2 sin 1A-2a, PTP35 r U40652 11 74.9.3.	1 10.3
x U60116 1 >100 r XLU37376 1 28.7 r RNU88958 1 1.8 r RNU88958 1 1.8 r U41853 1 9.3 r U41853 1 9.3 r Y1Z319 1 2.1 r Y1Z319 1 55.5 r M88136 3 2.4 m L13129 1 2.2 r M86195791 1 2.3 r U52945 2 2.2 r U40652 11 74.9.	1 38.4 N68
XLU37376	1 29.4
r RNU88958 1 1.8 r U41853 1 9.3 (PHF2)	
r regulated protein) r U41853 1 9.3 (PHE2) h NM 0053921 1 2.1 Sellar alaxia type 3 gene) r Y12319 1 55.5 m L13129 1 2.2 h R4F09591 1 2.2 h R709591 1 2.3 h R70	
(PHF2) bellar alaxia type 3 gene) r Y12319 1 55.5 m K12319 1 55.5 m K13129 1 2.2 m L13129 1 2.2 h AF095791 1 2.3 th D11ty protein) m U52945 2 2.2 -like protein 1A-2a; PTP35 r U40652 11 74.9.5;	1 7.8 R
bellar alaxia type 3 gene) r 712319 1 55.5 h M68136 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 n U52945 2 2.2 -like protein 1A-2a; PTP35 r U40652 11 74.9.5;	71 1 6.7 R
h M88136 3 2.4 m L13129 1 2.2 h AF095791 1 2.3 n U52945 2 2.2 -like protein 1A-2a; PTP35 r U40652 11 74.9.3	
m L13129 1 2.2 h AF095791 1 2.3 nbllity protein) m US2945 2 2.2 -like protein 1A-2a; PTP35 r U40652 11 74,9,5;	Servl tRN
h AF095791 1 2.3 nbllity protein) m US2945 2 2.2 like protein 1A-2a; PTP35 r U40652 11 74,9,5;	Synexin
m U52945 2 2.2 PTP35 r U40652 11 74.9	TACCS
PTP35 r U40652 11 74.9	TSG101 (t
	Tyrosine

Others

FIG. 2D



Expressed Sequence Tags (EST)

Up-adjusted ESTs	ESTAA066174 ESTAA925028 ESTAA07499 ESTAA043118 ESTAA17685 ESTAA045179 ESTAA17685 ESTAA0131015 ESTAA616986 ESTA1031015 ESTAA616986 ESTA1034161 ESTAA798953 ESTA1034161 ESTAA798953 ESTANO01070 ESTAA798953 ESTANO01070 ESTAA8010415 ESTWEO01070 ESTAA80112 ESTAA850112 ESTAA850123 ESTAA850124 ESTAA850126 ESTAA859425 ESTAA859425	lences	20 New Sequences
	ESTAA85947 ESTAA85944 ESTAA859740 ESTAA86364031 ESTAA891376 ESTAA899000 ESTAA890000 ESTAA890000 ESTAA901340 ESTAA901340 ESTAA901340 ESTAA901340 ESTAA901340 ESTAA901340 ESTAA901340 ESTAA901088	New Sequences	
Down-adjusted ESTs	ESTAA67476 ESTAA681418 ESTAA710096 ESTAA72531 ESTAA734740 ESTAA735120 ESTAA764153 ESTAA764153 ESTAA793073 ESTAA793073 ESTAA79100 ESTAA801125 ESTAA81125 ESTAA81125 ESTAA81125 ESTAA81125 ESTAA81125		25 New Sequences
Down-ad	ESTAA276763 ESTAA27606 ESTAA286128 ESTAA289129 ESTAA372927 ESTAA412823 ESTAA462855 ESTAA462855 ESTAA516974 ESTAA516974 ESTAA517260 ESTAA517339 ESTAA572112 ESTAA572112 ESTAA57650 ESTAA67711339 ESTAA677112 ESTAA677112		25 New
	ESTAA003402 ESTAA028510 ESTAA03320 ESTAA086565 ESTAA122792 ESTAA12450 ESTAA154450 ESTAA161894 ESTAA161894 ESTAA161894 ESTAA16029 ESTAA16029 ESTAA200452 ESTAA200452 ESTAA201114 ESTAA266966 ESTAA266966 ESTAA266966 ESTAA266966		

FIG. 2E



4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Express	ion St	Expression Strength	O constant	Expres	sion S	Expression Strength
Sequence identity (Genbank/EMBL)	208F	FE8	된 - 8 년 6	Sequence loemily (Genbank/EMBL)	208F	년 원	면 - 89 년
			+FD				47.0
3-hydroxy 3-methylglutaryl coA synthase	+++	+	+++	Bleomycin hydrolase	+	‡	++
ABP-280 (actin binding protein/filamin)	+	‡	+++	BRCA1-associated RING protein (Bard1)	0	‡	+
Alpha-actin	+++	+	+++	ElB 19K/Bcl-2-binding protein (Nip3)	0	+++	++
Antioxidant enzyme AOE372	‡	+	‡	Exportin	+	+++	+
AP56 (acetaminophen-binding protein)	‡	0	++	FEN-1 (flap endonuclease-1)	0	+++	+
Cdc21	‡	0	+++	FKBP51 (T-cell-specific immunophilia)	0	+++	+
Centromeric protein CENPC (a)	+++	0	‡	FLIP (FLICE-like inhibitory protein)	0	‡	0
Collagen alpha 1	+++	+	+++	GEF-H1	0	+++	+
CSF-1 (colony stimulating factor 1)	‡	0	+	LAPIC (lamina associated polypeptide 1)	0	† † †	0
DOC-2; p96 phosphoprotein	‡	0	+++	MAM domain protein	0	+++	+
FRS1 transcription factor	+++	+	++	MAP-kinase phosphatase (cpg21) (c)	0	+++	+
ETF transcription factor	+++	0	++	MMP-10 (Stromelysin-2) (d)	0	+++	0
Fibronectin	+ + +	+	+ + +	MMP-3 (Stromelysin-1)	0	+ + +	0
Follistatin-related protein; TSC36	‡	+	+++	Myb-binding protein (P160)	+	+++	+
GRP94/endoplasmin	+ + +	+	+++	NF-1 transcription factor	0	‡	0
Gu binding protein	++++	0	+	Non-neuronal enolase (NNE)	+	+++	‡
Heat shock protein 90	‡	0	‡	ORP150 (150 kDa oxygen regulated)	+	+++	+
HSPG core fibroglycan (syndecan-2)	+++	0	‡	p67 (isoprenylated 67 kDa protein)	0	+++	‡
Interferon induced gene	+ + +	0	‡	PkB kınase	0	+++	+
L1 retroposon (ORF2)	++++	0	‡	Rap1B GTP binding protein (e)	0	+++	+-
Laminin B1	+++	+	‡	Ras-GTPase-activating protein	0	+++	+
Lysyl oxidase	+ + +	0	+	Rsca3 (rat spinocerebellar ataxía gene)	0	+++	+
Lysyl oxidase-related protein (WS9-14)	‡	0	+	SA-1 (stromal antigen)	0	‡	+
Mama gene	+++	0	+	Sort1 (Sortilin)	0	+++	· ‡
MMP-2 (Gelatinase A)	+	0	+ + +	TSG101 (tumor susceptibility protein)	‡	+++	‡
mTFE3 (transcriptional activator)	‡	+	‡				
Nuclear autoantigen GS2NA	‡	0	+++				
Osteoglycin	‡	0	‡				
P5 protein	+++	+	‡				
P-cadherin	‡	0	+ + +				
Phosducin-like protein (PhLP)	+++	0	+				
Serum inducible kinase (SNK)	+++	0	‡				
STAT5al transcription factor	+	0	+++				
Thrombospondin 1	++++	0	+				
TIMP-2 (inhibitor of metalloproteinase 2)	++++	+	‡				
TRPM-2/clusterin (b)	+ + +	+	+ + +				

FIG. 3



	Exp	pressio	n Stre	ngth
Sequence Identity (Genbank/EMBL)	208F	FE-8 H-Ras	208F K-Ras	208F N-Ras
ABC transporter MOAT-B	0	++++	0	+
BCSC-1 (breast cancer suppressor candidate 1)	+	++++	0	+
Cyclooxygenase 1	+	++++	+	+++
E1B 19K/Bc1-2-binding protein (Nip3)	0	++	++++	++
EST AA743557	++++	+	. 0	++
EST AA792426	+	++++	+	+
EST AA924000	+	++++	+	++
ETF TEA domain containing transcription factor	++++	0	++	++
Famesyl pyrophosphate synthetase	+	+++	0	+
FEN-1 (flap endonuclease-1)	0	++++	+	0
FLIP (FLICE-like inhibitory protein)	0	+	++	++++
JAK1 protein tyrosine kinase 1	+	++++	+	+
MAGE-B gene cluster	0	++++	0	0
MAP-kinase phosphatase (cpg21)	0	++	+++	++++
MARCKS	++++	0	+	+++
MMP-10 (Stromelysin 2)	0	++	++	++++
Mob-1 (f)	0	++++	++	+
mTFE3 (X-linked transcriptional activator)	++++	0	+	+
Myb-binding protein (P160)	+	++++	++	++
novel transcript N317	++++	0	++	++++
P-cadherin (g)	++++	0	0	++
Phosphatidylinositol 3-kinase p170	+++	0	+	++
Ras-GTPase-activating protein	0	++++	0	0
SBF1 phosphatase	0	++++	+	+
Serum inducible kinase (SNK) (h)	++++	0	+++	+++
Tyrosine phosphatase IA-2a (i)	0	++++	0	++

FIG. 4



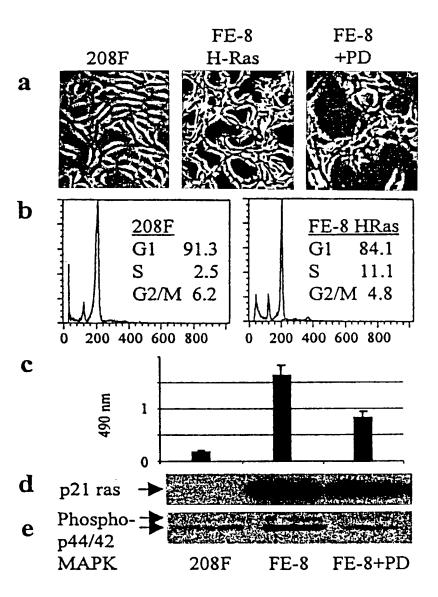


FIG. 5



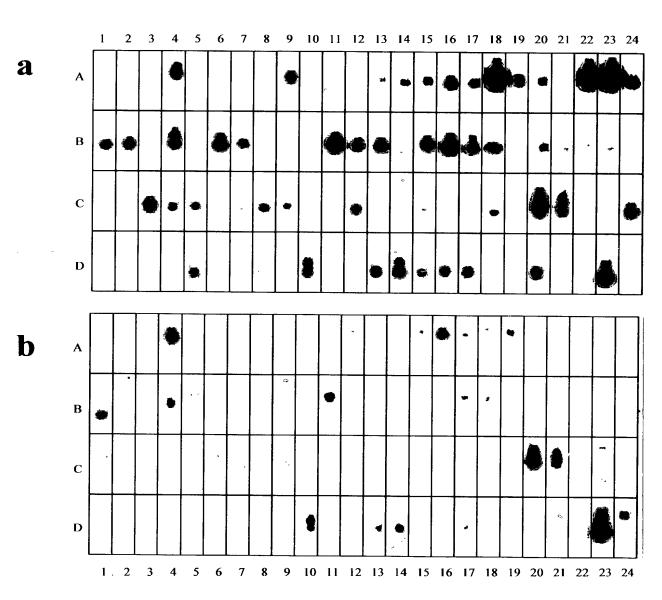
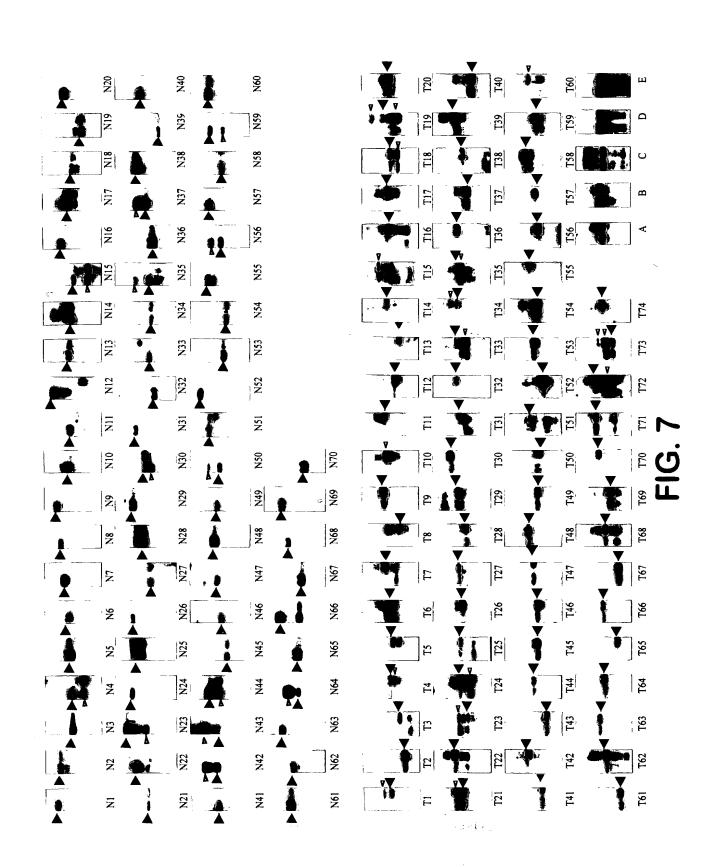


FIG. 6



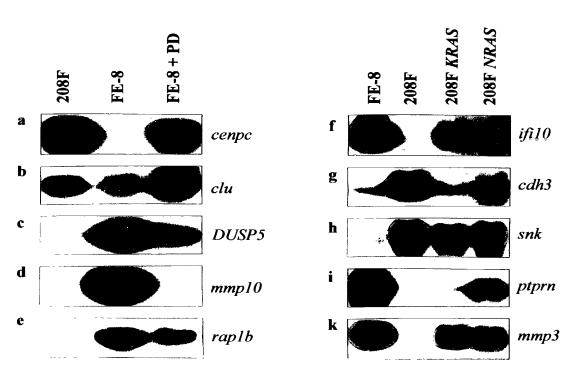


FIG. 8

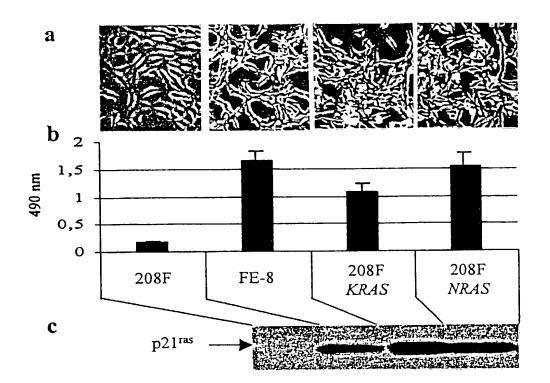


FIG. 9

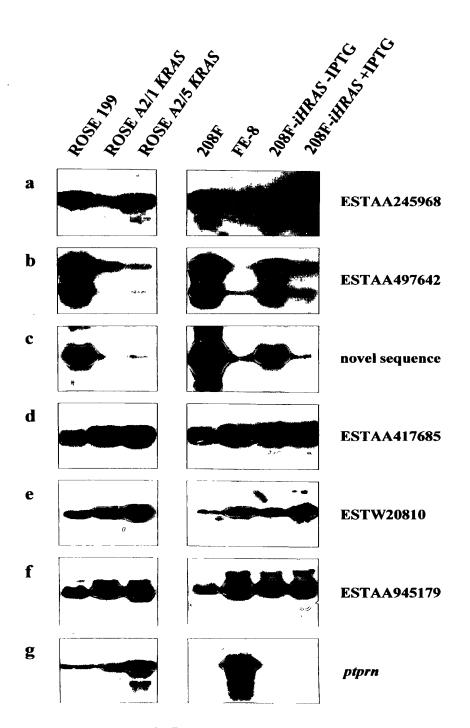


FIG. 10

```
1
    T59
Z
    T182
3
    T82
4
    T6
    T34
5
6
    N5
7
    NZO
    N280
9
    N271
10
     N126
11
     T148
     N199
12
13
     T64
14
     N131
15
     T20
16
     T162
17
     T141
18
     N77
19
     N104
20
     T49
21
     T16
22
     N189
23
     N28
24
     T124
25
     T216
26
     T60
     T37
27
28
     T160
29
     N101
30
     N40
31
     T54
32
     T120
33
     N159
34
     T185
35
     N151
36
     T147
37
     N188
38
     T25
39
     T47
40
     T43
     T139
41
42
     T176
43
     N144
44
     T35
     T98
45
46
     T15
47
     T138
46
     N21
49
     T76
50
     T103
51
     T143
52
     T44
53
     N31
54
     T243
55
     N129
56
     T193
57
     T132
58
     T137
59
     T217
60
     T191
```

62

N42

T156

FIG. 11



```
64
     N196
65
     T21
66
     N34
67
     N134
68
     T119
69
     N36
70
     N209
71
     N256
72
     T105
73
     T75
74
     T153
75
     T189
76
     TB6
77
     T111
78
     T144
79
     N192
80
     N103
81
     N270
82
     N255
83
     NGI
84
     N137
85
     T174
86
     N22
87
     T2
88
     T237
89
      T19
90
     N156
91
     N59
92
     N235
92
     N248
92
     N249
92
      N252
92
     N257
93
      8ET
94
      T121
95
      Nlo
96
      T129
97
      T66
98
      T36
99
      T40
100
       Nl
101
       N212
       T100
102
       N112
103
104
       ΝЗ
105
       N238
106
       T183
107
       T238
108
       T166
109
       N29
110
       T225
111
       N175
112
       N142
113
       T72
114
       N186
115
       T212
116
       T196
117
       T48
118
       N132
119
       N158
120
       T69
```

122

N7 T245 **FIG. 11A**



FIG. 11B



```
184
      N14
185
      N121
186
      T17
187
      TЗ
188
      T117
139
      T14
      T73
190
191
      N4
192
      N289
193
      T239
194
      T170
195
      T146
196
      N17
197
      T235
198
      N74
199
      N18
200
      T211
201
      T186
201
       T204
202
      N50
203
      N116
204
       T223
      и198
205
206
      N267
207
       T133
208
       T80
209
       N218
210
       N266
211
       T224
212
       N148
213
       N108
214
       N263
215
       N250
       N92
216
217
       N152
218
       T11
219
       T159
220
       N243
221
       N78
222
       T116
223
       T27
224
       N207
225
       TBI
226
       изв
227
       N163
228
       N81
229
       T94
230
       N228
231
       08N
232
       T230
233
       T188
234
       N130
235
       N187
236
       N136
237
       N294
238
       N275
239
       N65
240
       N89
241
       N125
242
       N205
243
       N39
244
       N13
```

T48

FIG. 11C



```
246
      T100
247
      T223
      N104
248
249
      N35
250
       T245
251
      N32
252
       T62
253
       N125
254
      N180
255
       N22
256
       T61
       T125
257
258
       T174
259
       T36
260
       T19
261
       T204
       T153
262
263
       T27
264
       T212
       T159
265
266
       T226
267
       T239
268
      N263
269
       T66
270
       N75
271
      N250
272
       T175
273
      N283
274
       T40
275
      N152
276
      N256
277
      N28
278
       T160
279
       T82
280
       N122
281
       T170
282
       N44
283
      N18
284
       T103
285
       N126
286
      N55
287
       T42
289
       T34
      N158
289
290
      N21
291
       N154
292
       081
293
       T189
294
       T17
295
       T68
296
       T14
297
       T146
298
       T120
299
       N181
300
      N192
301
       T109
302
      N215
303
       T244
303
       T251
304
       T96
305
       T211
306
       T243
```

N218

FIG. 11D



```
308
      T224
309
      T94
310
      T183
311
      N294
312
      T191
313
      T88
314
      T9
315
      N204
316
      N175
317
      N129
318
      T141
319
      N188
320
      N209
321
322
      T111
      T144
323
      N213
324
      N109
325
      N62
326
      T235
327
      N198
328
      N148
329
      N78
330
      T116
331
      N46
332
      N49
333
      N51
334
      N52
```

T26

FIG. 11E